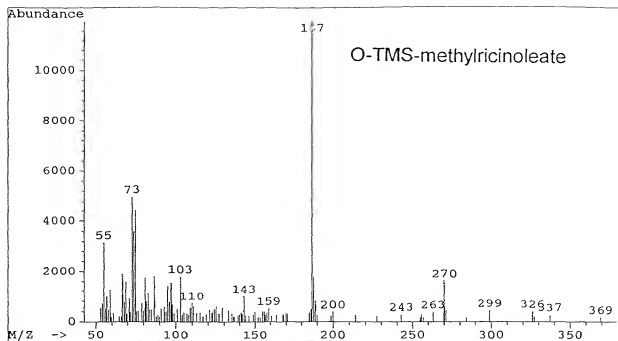
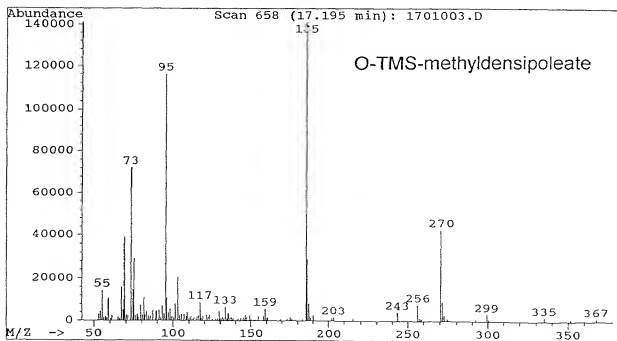


Figure 1A

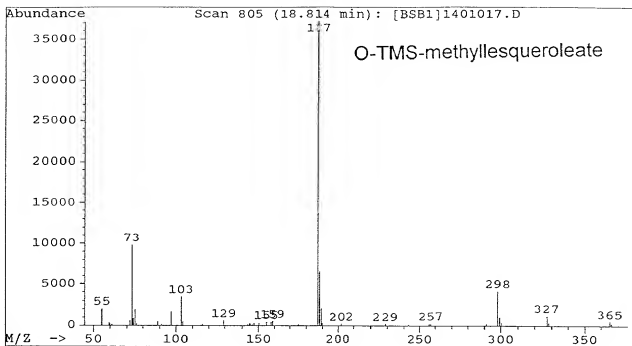


1B

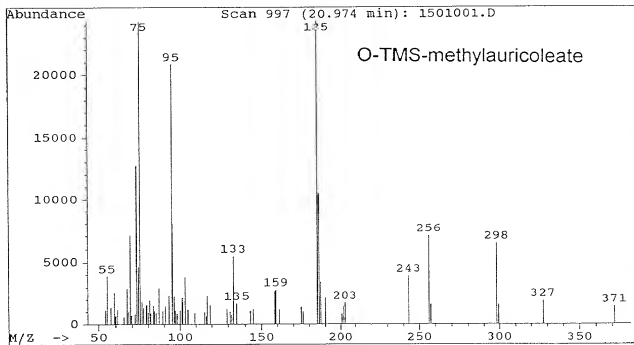


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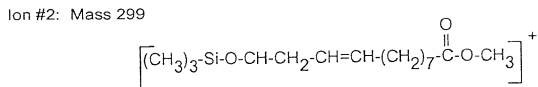
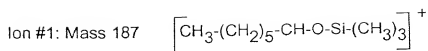
1C



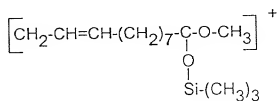
1D



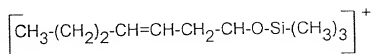
0000100-06101



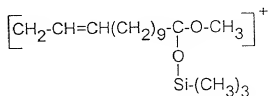
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of ion

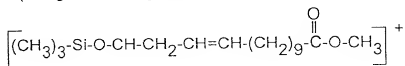


Figure 2

Figure 3

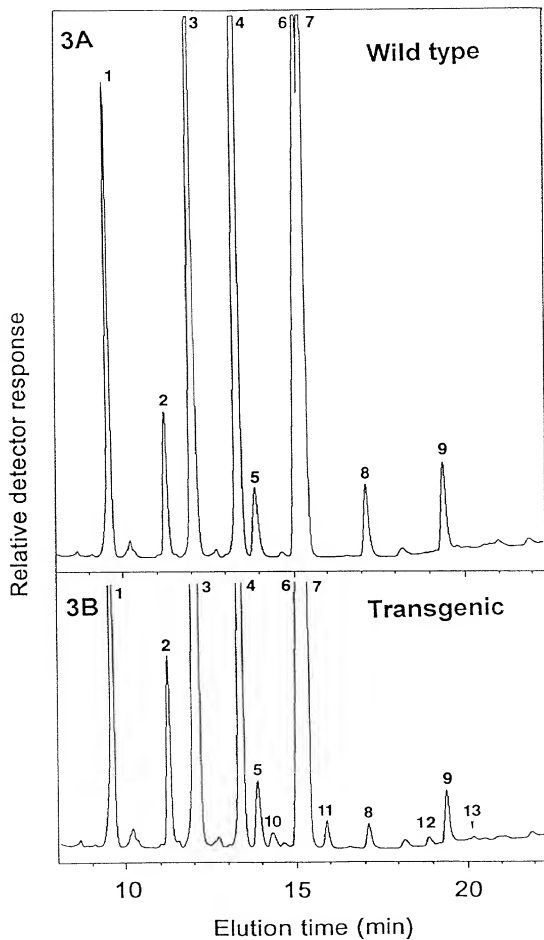
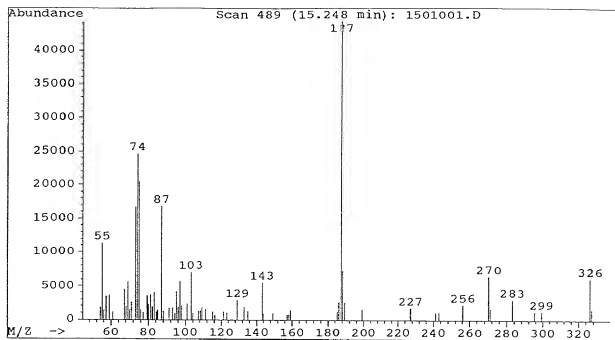
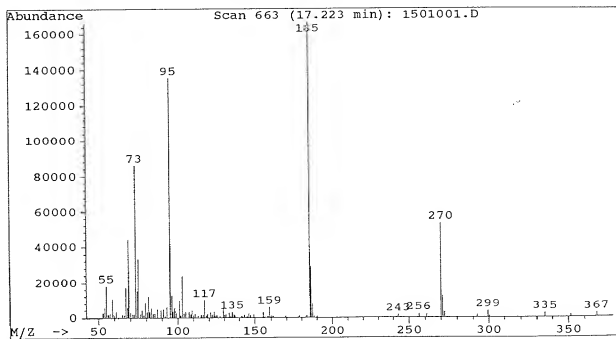


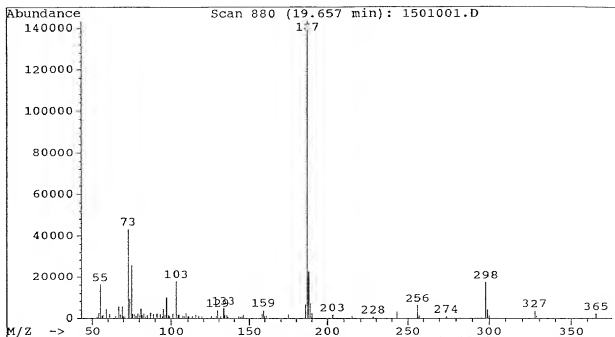
Figure 4A Mass spectrum of peak 10 from figure 3B



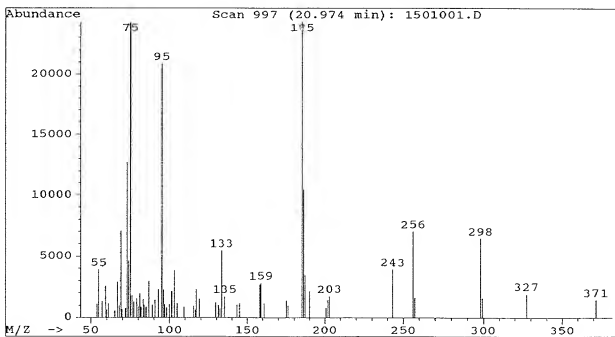
4B Mass spectrum of peak 11 from figure 3B



4C Mass spectrum of peak 12 from figure 3B



4D Mass spectrum of peak 13 from figure 3B



10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CAITTCCTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTTT	CCTTGTCTTG	GTCACITTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					

CAC

Figure 5

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAACTGTCCA	GTTTCGTCCTC	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGCTTGG	ATCACTTACT	TACAACACAC	TCACCTGCG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					

CACT

Figure 6

00005100-023104
101250-6815880

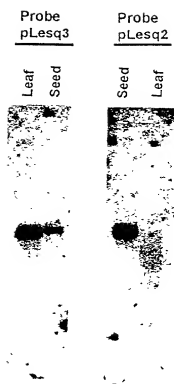


Figure 7

AT	GAA	GCT	TTA	TAA	GAA	GTT	AGT	TTT	CTC	TGG	TGA	CAG	AGA	AAT	TNT	47
GTC	AAT	TGG	TAG	TGA	CAG	TTG	AAG	CAA	CAG	GAA	CAA	CAA	GGA	TGG	TTG	95
GTG	NTG	ATG	CTG	ATG	TGG	TGA	TGT	GTT	ATT	CAT	CAA	ATA	CTA	AAT	ACT	143
ACA	TTA	CTT	GTT	GCT	GCC	TAC	TTC	TCC	TAT	TTC	CTC	CGC	CAC	CCA	TTT	191
TGG	ACC	CAC	GAN	CCT	TCC	ATT	TAA	ACC	CTC	TCT	CGT	GCT	ATT	CAC	CAG	239
AAG	AGA	AGC	CAA	GAG	AGA	GAG	AGA	GAG	AAT	GTT	CTG	AGG	ATC	ATT	GTC	287
TTC	TTC	ATC	GTT	ATT	AAC	GTA	AGT	TTT	TTT	TGA	CCA	CTC	ATA	TCT	AAA	335
ATC	TAG	TAC	ATG	CAA	TAG	ATT	AAT	GAC	TGT	TCC	TTC	TTT	TGA	TAT	TTT	383
CAG	CTT	CTT	GAA	TTC	AAG	Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	10431
Pro	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Glu	Ala	Leu	Lys	Arg	Gly	Pro	Cys	26479
CCC	TCT	TCC	AAG	AAA	TCA	GAA	ACT	GAA	GCC	CTA	AAA	CGT	GGA	CCA	TGT	
Glu	Lys	Pro	Pro	Phe	Thr	Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	42527
GAG	AAA	CCA	CCA	TTC	ACT	GTT	AAA	GAT	CTG	AAG	AAA	GCA	ATC	CCA	CAG	
His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	58575
CAT	TGT	TTT	AAG	CGC	TCT	ATC	CCT	CGT	TCT	TCT	THC	TCC	TAU	CTT	ACA	
Asp	Ile	Thr	Leu	Val	Ser	Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	74623
GAT	ATC	ACT	TTA	GTT	TCT	TGC	TTC	TAC	TAC	GTT	GCC	ACA	AAT	TAC	TTC	
Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	90671
TCT	CTT	CTT	CCT	CAG	CCT	CTC	TCT	ACT	TAC	CTA	GCT	TGG	CCT	CTC	TAT	
Trp	Val	Cys	Gln	Gly	Cys	Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	106719
TGG	GTA	TGT	CAA	GGC	TGT	GTC	TTA	ACC	GGT	ATC	TGG	GTC	ATT	GGC	CAT	
Glu	Cys	Gly	His	His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	122767
GAA	TGT	GGT	CAT	CAT	GCA	TTC	AGT	GAC	TAT	CAA	TGG	GTA	GAT	GAC	ACT	
Val	Gly	Phe	Ile	Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	138815
GTT	GGT	TTT	ATC	TTC	CAT	TCC	TTC	CTT	CTC	GTC	CCT	TAC	TTC	TCC	TGG	
Lys	Tyr	Ser	His	Arg	Arg	His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	154863
AAA	TAC	AGT	CAT	CGT	CGT	CAC	CAT	TCC	AAC	AAT	GGA	TCT	CTC	GAG	AAA	
Asp	Glu	Val	Phe	Val	Pro	Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	170911
GAT	GAA	GTC	TTT	GTC	CCA	CCG	GAG	AAA	GCT	GCA	GTC	AAA	TGG	TAT	GTT	
Lys	Tyr	Leu	Asn	Asn	Pro	Lys	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	186956
AAA	TAC	CTC	CAA	ACC	CCT	CTT	GGG	CGC	ATC	CTG	GTC	TTA	ACA	GTT	CAG	

Figure 8A

Pro CCT	Tyr TAT	Asp GAT	Gly GGT	Phe TTC	Ala GCT	Ser TCA	His CAT	Phe TTC	Phe TTC	Pro CCT	His CAT	Ala GCA	Pro CCT	Ile ATC	Phe TTT	202 1007
Lys AAA	Asp GAC	Glu CGA	Ala GAA	Gly CGC	Leu CTC	Leu CAG	Tyr ATA	Tyr TAC	Ala ATC	Ala TTC	Asn GCA	Val GCT	Ser GGT	Gly ATT	Arg CTA	218 1055
Ala GCT	Val GTC	Cys TGT	Tyr TAT	Gly GGT	Leu CTT	Tyr TAC	Arg CGT	Tyr TAC	Ala GCT	Ala GCT	Ser TCA	Gln CAA	Gly GGA	Leu TTG	Thr ACT	234 1103
Ala GCT	Met ATG	Ile ATC	Cys TGC	Val GTC	Tyr TAT	Gly GGA	Val GTA	Pro CCG	Leu CTT	Leu TTG	Ile ATA	Val GTG	Asn AAC	Phe TTT	Phe TTC	250 1151
Leu CTT	Val GTC	Leu TTG	Val GTA	Thr ACT	Phe TTC	Leu TTG	Gln CAG	His CAC	Thr ACT	His CAT	Pro CCT	Ser TCG	Leu TTA	Pro CCT	His CAT	266 1199
Tyr TAT	Asp GAT	Ser TCA	Thr ACC	Glu GAG	Trp TGG	Glu GAA	Trp TGG	Ile ATT	Arg AGA	Gly GGA	Ala GCT	Leu TTG	Val GTT	Thr ACG	Val GTA	282 1247
Asp GAC	Arg AGA	Asp GAC	Tyr TAT	Gly GGA	Ile ATA	Leu TTG	Asn AAG	Lys AAG	Val PHE	Phe TTC	His CAT	Asn AAC	Ile ATA	Thr ACA	Asp GAC	298 1295
Thr ACA	His CAT	Val GTG	Ala GCT	His CAT	His CAT	Leu CTC	Phe TTT	Ala GCA	Thr ACT	Ile ATA	Pro CCG	His CAT	Tyr TAT	Asn AAC	Ala GCA	314 1343
Met ATG	Glu GAA	Ala GCT	Thr ACA	Glu GAG	Ala GCG	Ile ATA	Lys AAG	Pro CCA	Ile ATA	Leu CTT	Gly GGT	Asp GAT	Tyr TAC	Tyr TAC	His CAC	330 1391
Phe TTC	Asp GAT	Gly GGA	Thr ACA	Pro CCG	Trp TGG	Tyr TAT	Val GTG	Ala GCC	Met ATG	Tyr TAT	Arg AGG	Glu GAA	Ala GCA	Lys AAG	Glu GAG	346 1439
Cys TGT	Leu CTC	Tyr TAT	Val GTA	Glu GAA	Pro CCG	Asp GAT	Thr ACG	Glu GAA	Arg CGT	Gly GGG	Lys AAG	Lys AAA	Gly GGT	Val GTC	Tyr TAC	362 1487
Tyr TAT	Tyr TAC	Asn AAC	Asn AAT	Lys AAG	Leu TTA	TGA	GGC	TGA	TAG	GGC	GAG	AGA	AGT	GCA	ATT	378 1535
ATC TTT	AAT GTT	CTT TCA	CAT ATA	TTC ATC	CAT TCA	GTT GAG	TTA ATN	GGT TAG	GTG TTG	TTT TGT	AAG TCT	AAG GGT	CTA GCA	TGC TTT		384 1583
TGC GTG	CTA CTG	GTT CCC	ATG AGT	TGG GAA	TGT GAA	CGG CAA	AAG GTT	TTA TAC	GTG GTG	TTC TTT	AAA AAA	CTG ATA	CTT CTC	GCT GGA		1631 1679
GTG AAT	CTG TGA	CCC CCA	AGT CAA	GAA NAT	GAA ATC	CAA AAC	CAA CGG	GTT CTA	TAC TCC	TTT GAA	AAA TTC	ATA CAT	CTC ATC	GGA CGA		1727 1775
AAA GAT	CGG ATC	GAT CAA	ATC ATT	ATC TCC	CAA AGA	ATT GTA	TCC CTT	AGA AG	GTA AG	CTT AG						1823 1855

Figure 8B

		10	20	30	40	50	
LFFAH12	1	MGAGGRIM--	--VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50
FAH12	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKKAIPPHC	50
ATFAD2	1	MGAGGRMP--	--VPTSSKKS	--ETDTRKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2	1	MGAGGRMO--	--VSPPSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
GMFAD2-1	1	MGLA-KETTM	GGRGRVAKVE	VQGGKPLSRV	PNTKPPFTVG	QLKKAIPPHC	50
GMFAD2-2	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPQFSLS	QIKKAIPPHC	50
ZMFAD2	1	MGAGGRMTEK	EREKQEOLAR	ATGGAAMORS	PVEKPPFTLG	QIKKAIPPHC	50
RCFAD2	1	-----	-----	-----	-----	-----	50
		60	70	80	90	100	
LFFAH12	51	FKRSIPRSFS	YLLTDITLVS	CFYYVATNYF	SLLPOPLSTY	LAWPLYWVCQ	100
FAH12	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVLWLFQ	100
ATFAD2	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPOPLS-Y	LAWPLYWACQ	100
BNFAD2	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAMPLYWACQ	100
GMFAD2-1	51	FQRLSLTSFS	YVVYDLSFAF	IFY-IATTYF	HLLPOPS-L	IAPWYIWLQ	100
GMFAD2-2	51	FORSVLRSFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-L	RGMAIYWAVQ	100
ZMFAD2	51	FERSVLKSFS	YVVHDLVIAA	ALLYFALAII	PALPSPLR-Y	AAMPLYWIAQ	100
RCFAD2	51	-----	-----	-----	-----	-----	100
		110	120	130	140	150	
LFFAH12	101	GCVLTGIWVI	GHECGHHAFS	DYQWDDTVG	FIFHSFLLVP	YFSWKYSHRR	150
FAH12	101	GCILTLGLWVI	GHECGHHAFS	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR	150
ATFAD2	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
BNFAD2	101	GCVLTGVWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
GMFAD2-1	101	GCLLTGVWVI	AHECGHHAFS	KYQWDDVVG	LTLHSTLLVP	YFSWKYSHRR	150
GMFAD2-2	101	GCILTLGVWVI	AHECGHHAFS	DYQLDDDIVG	LILHSALLVP	YFSWKYSHRR	150
ZMFAD2	101	G-----	-----AFS	DYSLDDVVG	LVLHSSLMVP	YFSWKYSHRR	150
RCFAD2	101	-----WVM	AHDCGHHAFS	DYQLDDVVG	LILHSCLLVP	YFSWKYSHRR	150
		160	170	180	190	200	
LFFAH12	151	HHSNNGSLEK	DEVFVPKKA	AVKWYVKYL-	NNPLGRILVL	TVOQFILGWPL	200
FAH12	151	HHSNIGSLER	DEVFVPKKS	KISWYSKYS-	NNPPGRVLT	AATLLGLWPL	200
ATFAD2	151	HHSNTGSLER	DEVFVPKQS	AIKWYKYL-	NNPLGRIMML	TVOQFVLGWPL	200
BNFAD2	151	HHSNTGSLER	DEVFVPR-RS	OTSSGTAST-	STTFGRVTML	TVOQFTLGWPL	200
GMFAD2-1	151	HHSNTGSLDR	DEVFVPKPS	KVAFWSKYL-	NNPLGRAVSL	LVTLTIGWPM	200
GMFAD2-2	151	HHSNTGSLER	DEVFVPKQS	CIKWYSKYL-	NNPPGRVLT	AVTLTLGWPL	200
ZMFAD2	151	HHSNTGSLER	DEVFVPKKE	ALPWYTPVY	NNPVGRVRI	VVQLTLGWPL	200
RCFAD2	151	HHSNTGSLER	DEVFVPKKS	SIRWYSKYL-	NNPPGRIMTI	AVTLSLGWPL	200
		210	220	230	240	250	
LFFAH12	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR	250
FAH12	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFFVLYQ	250
ATFAD2	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLSDAG	ILAVCYGLYR	250
BNFAD2	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP	250
GMFAD2-1	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSQVA	LFSYTYSLYR	250
GMFAD2-2	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYSORE	RLQIYISDAG	VLAVVYGLFR	250
ZMFAD2	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK	250
RCFAD2	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAVTFGLYQ	250

Figure 9A

		260	270	280	290	300	
LFFAH12	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLTFT	LQHTHPSLPH	YDSSEWEWIR	300
FAH12	251	ATMAKGLAWV	MRIYGVPLLI	VNCFVLMITY	LQHTHPAIPR	YGSSEWDWLR	300
ATFAD2	251	YAAAQGMASH	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
BNFAD2	251	YAAVQGVASH	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
GMFAD2-1	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHPALPH	YDSSEWDWLR	300
GMFAD2-2	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITY	LQHTHPALPH	YDSSEWDWLR	300
ZMFAD2	251	LAAGVGVWV	VRVYAVPLLI	VNAWLVLTITY	LQHTHPSLPH	YDSSEWDWLR	300
RCFAD2	251	LAIKGLAWV	VCVYGVPLLV	VNSFLVLITY	LQHTHPALPH	YDSSEWDWLR	300
		310	320	330	340	350	
LFFAH12	301	GALVTVDORDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12	301	GAMVTVDORDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYNAME	ATKAIKPIMG	350
ATFAD2	301	GALATVDORDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2	301	GALATVDORDY	GILNOGFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
GMFAD2-1	301	GALATMDORDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
GMFAD2-2	301	GALATVDORDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
ZMFAD2	301	GALATMDORDY	GILNRVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIRPILG	350
RCFAD2	301	GALATVDORDY	GILNKVFHNI	TDTHVAHHLF	-----	-----	350
		360	370	380	390	400	
LFFAH12	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVVYYNN	K-L.....	400
FAH12	351	EYYRYDGTTPF	YKALWREAKE	CLFVEPDDEGA	PTOGVFWYNN	KY-.....	400
ATFAD2	351	DYYQFDGTPW	YVAMYREAKE	CLYVEPDREG	DKKGVVYYNN	K-L.....	400
BNFAD2	351	EYYQFDGTPV	VKAMWREAKE	CLYVEPDREQ	EKKGVFWYNN	KL*.....	400
GMFAD2-1	351	EYYQFDGTPF	YKALWREAKE	CLYVEPDEGT	SEKGVFWYNN	KY-.....	400
GMFAD2-2	351	EYYRFDETTPF	VKAMWREAKE	CLYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2	351	DYYHFDTPPV	AKATWREAKE	CLYVEPE---	DRKGVFWYNN	KF*.....	400

Figure 9B

0985189-052104
101290-6815880

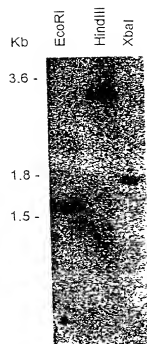


Figure 10

Plasmid size: 25.70 kb

Constructed by: Jonathon Jones

Construction date: 1992

Comments/References: Transgenic Research 1,285-297 (1992)

Figure 11

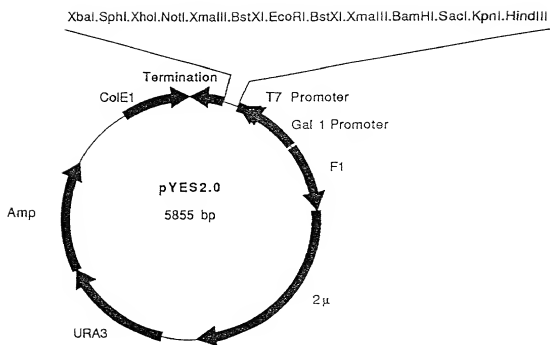


Figure 12

0906187 062101
101290 6815860

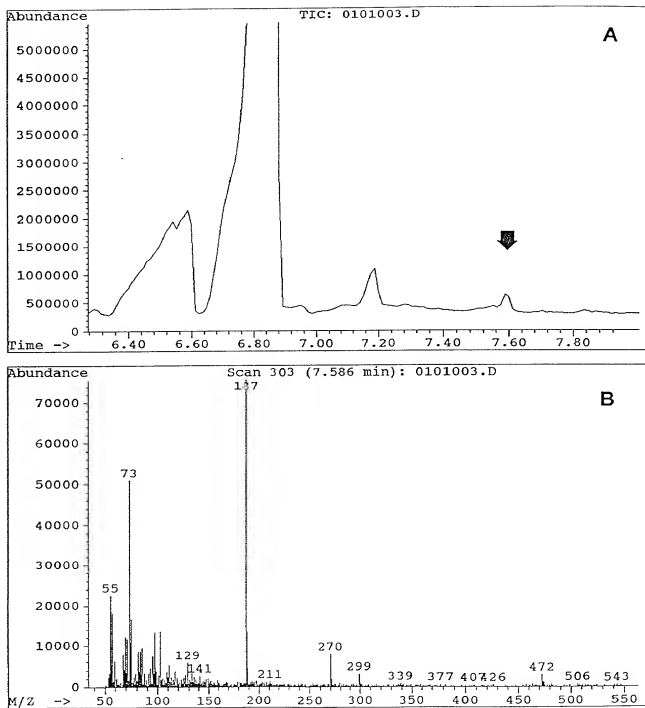


Figure 13